Supplementary Table 11. Genome-wide significant associations (P < 5 x 10-8) between SNPs and AUDIT-P ordered by chromosomal location.

|         |                    |            | AUDIT-P                |
|---------|--------------------|------------|------------------------|
| hromoso | on rsID earest Ger | <b>A</b> 1 | Beta (S.E.) P          |
| 4p14    | rs11940694 KLB     | G          | .007 (0.0011.1 x 10-9  |
| 4p23    | s14678803 METAP1   | G          | 0.04 (0.0011.2 x 10-9  |
| 4q23    | rs1229984' ADH1B   | С          | ).04 (0.0031.0 x 10-45 |
| 4q23    | 's1173369t ADH6    | Α          | 0.04 (0.0067.7 x 10-13 |
| 4q24    | 's13135092 SLC39A8 | G          | 0.01 (0.0024.5 x 10-15 |

Genes are listed if located within +/- 10kb of a listed SNP. A1=effect allele